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Range: from to Features: ☒ CDD

☐ 1: [NP_416275](#). Reports glutamate dehydro...[gi:16129715]

BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS NP_416275 447 aa linear BCT 27-JAN-2009
DEFINITION glutamate dehydrogenase, NADP-specific [Escherichia coli str. K-12 substr. MG1655].
ACCESSION NP_416275
VERSION NP_416275.1 GI:16129715
DESOURCE REFSEQ: accession NC_000913.2
KEYWORDS .
SOURCE Escherichia coli str. K-12 substr. MG1655
ORGANISM *Escherichia coli* str. K-12 substr. MG1655
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1 (residues 1 to 447)
AUTHORS Riley, M., Abe, T., Arnaud, M.B., Berlyn, M.K., Blattner, F.R., Chaudhuri, R.R., Glasner, J.D., Horiuchi, T., Keseler, I.M., Kosuge, T., Mori, H., Perna, N.T., Plunkett, G. III, Rudd, K.E., Serres, M.H., Thomas, G.H., Thomson, N.R., Wishart, D. and Wanner, B.L.
TITLE Escherichia coli K-12: a cooperatively developed annotation snapshot--2005
JOURNAL Nucleic Acids Res. 34 (1), 1-9 (2006)
PUBMED 16397293
REMARK Publication Status: Online-Only

REFERENCE 2 (residues 1 to 447)
AUTHORS Blattner, F.R., Plunkett, G., Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
TITLE The complete genome sequence of Escherichia coli K-12
JOURNAL Science 277 (5331), 1453-1474 (1997)
PUBMED 9278503

REFERENCE 3 (sites)
AUTHORS Kang, W.K., Icho, T., Isono, S., Kitakawa, M. and Isono, K.
TITLE Characterization of the gene rimK responsible for the addition of glutamic acid residues to the C-terminus of ribosomal protein S6 in Escherichia coli K12
JOURNAL Mol. Gen. Genet. 217 (2-3), 281-288 (1989)
PUBMED 2570347

REFERENCE 4 (residues 1 to 447)
AUTHORS Arnaud, M., Berlyn, M.K.B., Blattner, F.R., Galperin, M.Y., Glasner, J.D., Horiuchi, T., Kosuge, T., Mori, H., Perna, N.T., Plunkett, G. III, Riley, M., Rudd, K.E., Serres, M.H., Thomas, G.H. and Wanner, B.L.
TITLE Workshop on Annotation of Escherichia coli K-12
JOURNAL Unpublished
REMARK Woods Hole, Mass., on 14-18 November 2003 (sequence corrections)

REFERENCE 5 (residues 1 to 447)
AUTHORS Glasner, J.D., Perna, N.T., Plunkett, G. III, Anderson, B.D., Bockhorst, J., Hu, J.C., Riley, M., Rudd, K.E. and Serres, M.H.
TITLE ASAP: Escherichia coli K-12 strain MG1655 version m56

JOURNAL Unpublished
REMARK ASAP download 10 June 2004 (annotation updates)
REFERENCE 6 (residues 1 to 447)
AUTHORS Hayashi,K., Morooka,N., Mori,H. and Horiuchi,T.
TITLE A more accurate sequence comparison between genomes of *Escherichia coli* K12 W3110 and MG1655 strains

JOURNAL Unpublished
REMARK GenBank accessions AG613214 to AG613378 (sequence corrections)
REFERENCE 7 (residues 1 to 447)
AUTHORS Perna,N.T.
TITLE *Escherichia coli* K-12 MG1655 yqiK-rfaE intergenic region, genomic sequence correction

JOURNAL Unpublished
REMARK GenBank accession AY605712 (sequence corrections)
REFERENCE 8 (residues 1 to 447)
AUTHORS Rudd,K.E.
TITLE A manual approach to accurate translation start site annotation: an *E. coli* K-12 case study

JOURNAL Unpublished
REFERENCE 9 (residues 1 to 447)
CONSRM NCBI Genome Project
TITLE Direct Submission

JOURNAL Submitted (27-JAN-2009) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
REFERENCE 10 (residues 1 to 447)
AUTHORS Rudd,K.E.
TITLE Direct Submission

JOURNAL Submitted (22-DEC-2008) Department of Biochemistry and Molecular Biology, University of Miami Miller School of Medicine, 118 Gautier Bldg., Miami, FL 33136, USA
REMARK Annotation update from ecogene.org as a multi-database collaboration

REFERENCE 11 (residues 1 to 447)
AUTHORS Rudd,K.E.
TITLE Direct Submission

JOURNAL Submitted (12-MAR-2008) Department of Biochemistry and Molecular Biology, University of Miami Miller School of Medicine, 118 Gautier Bldg., Miami, FL 33136, USA
REMARK Annotation update from ecogene.org as a multi-database collaboration

REFERENCE 12 (residues 1 to 447)
AUTHORS Rudd,K.E.
TITLE Direct Submission

JOURNAL Submitted (26-SEP-2007) Department of Biochemistry and Molecular Biology, University of Miami Miller School of Medicine, 118 Gautier Bldg., Miami, FL 33136, USA
REMARK Annotation update from ecogene.org as a multi-database collaboration

REFERENCE 13 (residues 1 to 447)
AUTHORS Rudd,K.E.
TITLE Direct Submission

JOURNAL Submitted (24-APR-2007) Department of Biochemistry and Molecular Biology, University of Miami Miller School of Medicine, 118 Gautier Bldg., Miami, FL 33136, USA
REMARK Annotation update from ecogene.org as a multi-database collaboration

REFERENCE 14 (residues 1 to 447)
AUTHORS Plunkett,G. III.
TITLE Direct Submission

JOURNAL Submitted (07-FEB-2006) Laboratory of Genetics, University of Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
REMARK Protein updates by submitter

REFERENCE 15 (residues 1 to 447)
AUTHORS Plunkett,G. III.

TITLE Direct Submission
 JOURNAL Submitted (10-JUN-2004) Laboratory of Genetics, University of Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
 REMARK Sequence update by submitter
 REFERENCE 16 (residues 1 to 447)
 AUTHORS Plunkett,G. III.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
 REFERENCE 17 (residues 1 to 447)
 AUTHORS Blattner,F.R. and Plunkett,G. III.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-1997) Laboratory of Genetics, University of Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
 REFERENCE 18 (residues 1 to 447)
 AUTHORS Blattner,F.R. and Plunkett,G. III.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1997) Laboratory of Genetics, University of Wisconsin, 425G Henry Mall, Madison, WI 53706-1580, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AAC74831. Method: conceptual translation.
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 /db_xref="taxon:511145"
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 /EC_number="1.4.1.4"
 /function="enzyme; Amino acid biosynthesis: Glutamate"
 /calculated_mol_wt=48450
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 /note="glutamate dehydrogenase; Provisional; PRK09414"
 /db_xref="CDD:103887"
 Region 57..187
 /region_name="ELFV dehydrog N"
 /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain; pfam02812"
 /db_xref="CDD:111682"
 Region 202..445
 /region_name="NADB_Rossmann"
 /note="Rossmann-fold NAD(P)(+)-binding proteins; c10931"
 /db_xref="CDD:127283"
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 /locus_tag="b1761"
 /gene_synonym="ECK1759"
 /gene_synonym="JW1750"
 /coded_by="NC_000913.2:1840395..1841738"
 /experiment="N-terminus verified by Edman degradation: PMID 6308576, 9298646"
 /GO_component="GO:0005737 - cytoplasm"
 /GO_process="GO:0006537 - glutamate biosynthetic process"
 /note="NADP-specific glutamate dehydrogenase"
 /transl_table=11
 /db_xref="ASAP:ABE-0005865"
 /db_xref="UniProtKB/Swiss-Prot:P00370"
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 /db_xref="GeneID:946802"



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121 tlpmgggkgg sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
181 gmmkklsnnt acvftgkgl fggslirpea tgyglvyfte amlkrhgmff egmrsvsags
241 gnvagyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
301 glvyleggqp wslpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
361 qagvlfapgg aanaggvats glemaqnaar lgwkaekvda rlhhimldih hacvehggeg
421 eqtnyvqgan iagfvkvada mlaqgvi
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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to Features: ☒ CDD

☐ 1: [AAA23868](#). Reports glutamate dehydro...[gi:146126]

BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS AAA23868 447 aa linear BCT 26-APR-1993

DEFINITION glutamate dehydrogenase.

ACCESSION AAA23868

VERSION AAA23868.1 GI:146126

DBSOURCE locus ECOGDHAK accession [K02499.1](#)

KEYWORDS

SOURCE Escherichia coli

ORGANISM [Escherichia coli](#)

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE 1 ([residues 1 to 447](#)).

AUTHORS Valle, F., Becerril, B., Chen, E., Seeburg, P., Heyneker, H. and Bolivar, F.

TITLE Complete nucleotide sequence of the glutamate dehydrogenase gene from Escherichia coli K-12

JOURNAL Gene 27 (2), 193-199 (1984)

PUBMED [6373501](#)

COMMENT [1] notes a potential ribosome binding site at 178-182.

Method: conceptual translation.

FEATURES Location/Qualifiers

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/db_xref="taxon:562"

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/name="glutamate dehydrogenase"

6..447

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/note="glutamate dehydrogenase; Provisional; PRK09414"

/db_xref="CDD:103887"

57..187

/region_name="ELFV_dehydrog_N"

/note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;

pfam02812"

/db_xref="CDD:111682"

202..445

/region_name="NADB_Rossmann"

/note="Rossmann-fold NAD(P) (+)-binding proteins; cl09931"

/db_xref="CDD:127283"

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/transl_table=11

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121 tlpmgggkqg sddpdkgkxe gevmrfcqal mtelyrhlg dtdvpagdig vggrevgfma
181 gmmkklsnnt acvftgkgl fggslirpea tgyglvyfte amlkrhgmfg egmrsvsvgs
241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rliekasrd grvadyakef



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301 glvyleggqp wslpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfg
361 gagvlfapggk aanaggvats glempqnaar lgwkaekvda rlhhimldih hacvehggeg
421 eqtnyvqgan iagfvkvada mlaqgvi
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Range: from to Features: ☒ CDD

☐ 1: NP_288194. Reports glutamate dehydro...[gi:15802172]

BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS NP_288194 447 aa linear BCT 18-JUL-2008
 DEFINITION glutamate dehydrogenase [Escherichia coli O157:H7 EDL933].
 ACCESSION NP_288194
 VERSION NP_288194.1 GI:15802172
 DBSOURCE REFSEQ: accession NC_002655.2
 KEYWORDS .
 SOURCE Escherichia coli O157:H7 EDL933
 ORGANISM Escherichia coli O157:H7 EDL933
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 447)
 AUTHORS Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
 Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
 Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
 Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamouisis,K.,
 Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
 Welch,R.A. and Blattner,F.R.
 TITLE Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
 JOURNAL Nature 409 (6819), 529-533 (2001)
 PUBMED 11206551
 REFERENCE 2 (residues 1 to 447)
 CONSRM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-2001) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (residues 1 to 447)
 AUTHORS Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
 Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
 Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
 Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamouisis,K.,
 Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
 Welch,R.A. and Blattner,F.R.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-2000) Laboratory of Genetics, University of
 Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from AAG56747.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /strain="EDL933"
 /serotype="O157:H7"
 /db_xref="taxon:155864"
 /note="enterohemorrhagic"
 Protein 1..447
 /product="glutamate dehydrogenase"
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/calculated_mol_wt=48438
Region 6..447
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/note="glutamate dehydrogenase; Provisional; PRK09414"
/db_xref="CDD:103887"
Region 57..187
/region_name="ELFV_dehydrog_N"
/note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
pfam02812"
/db_xref="CDD:111682"
Region 202..445
/region_name="NADB_Rossmann"
/note="Rossmann-fold NAD(P) (+)-binding proteins; cl09931"
/db_xref="CDD:127283"
CDS 1..447
/gene="gdhA"
/locus_tag="Z2793"
/coded_by="NC_002655.2:2517086..2518429"
/note="converts 2-oxoglutarate to glutamate; in
Escherichia coli this enzyme plays a role in glutamate
synthesis when the cell is under energy restriction; uses
NADPH; forms a homoheptamer"
/transl_table=11
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ORIGIN

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1 mdtyslesf lnhvqkrdpn qtefaqavre vmttlwpfle qnpkyrqmsl lerlveperv
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121 tlpmgggkgs sdfdpkgkse gevmrfcqal mtelyrhlga dtdvpagdig vggrevgfma
181 gmmkklsntt acvftgkgl fggslirpea tgyglvyfte amkrhgmgi egmrvsvgs
241 gnvagyaiek amefgarvit asdssgtvvd esgftkekla rlieikssrd grvadyakef
301 glvylegqgp wsvpdialp catqnelddv aahqliangv kavaeganmp ttieatelfq
361 qagvlfagpk aanaggvats glemagnaar lgwkaekvda rlhhimldih hacvehggeg
421 eqtnyvqqan iagfvkvada mlaqqvi

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Range: from to Features: ☒ CDD

BLINK, Conserved
Domains, Links

☐ 1: [NP_754056](#). Reports [glutamate dehydro...](#) [gi:26248016]

Comment Features Sequence

LOCUS NP_754056 447 aa linear BCT 20-JUL-2008
 DEFINITION glutamate dehydrogenase [Escherichia coli CFT073].
 ACCESSION NP_754056
 VERSION NP_754056.1 GI:26248016
 DBSOURCE REFSEQ: accession [NC_004431.1](#)
 KEYWORDS
 SOURCE
 ORGANISM [Escherichia coli CFT073](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE
 AUTHORS 1 ([residues 1 to 447](#))
 Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
 Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
 Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
 Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
 TITLE Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
 PUBMED [12471157](#)
 REFERENCE
 AUTHORS 2 ([residues 1 to 447](#))
 NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted ([10-SEP-2004](#)) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 REFERENCE
 AUTHORS 3 ([residues 1 to 447](#))
 Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
 Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
 Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
 Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) Genetics Laboratory, University of
 Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [AAN80621](#).
 Method: conceptual translation.
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 /db_xref="taxon:199310"
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 /EC_number="1.4.1.4"
 /function="enzyme; Amino acid biosynthesis: Glutamate"
 /calculated_mol_wt=48438
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        /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain; pfam02812"
        /db_xref="CDD:111682"
Region 202..445
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        /note="Rossmann-fold NAD(P) (+)-binding proteins; cl09931"
        /db_xref="CDD:127283"
CDS 1..447
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        /coded_by="NC_004431.1:1996215..1997558"
        /note="converts 2-oxoglutarate to glutamate; in Escherichia coli this enzyme plays a role in glutamate synthesis when the cell is under energy restriction; uses NADPH; forms a homohexamer"
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    181 gmmkklsnnt acvftgkgl fggslirpea tgyglvyfte amlkrhgmfg egmrsvsvgs
    241 gnvaqyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
    301 glvylegqqp wsvpdialp catqnelvdv aahqliangv kavaeganmp ttieatelfq
    361 qagvlfapgk aanaggvats glemagnaar lgwkaekvda rlhhimldih hacvehggeg
    421 eqtnyvqgan iagfvkvada mlsqgvi
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Range: from to Features: ☒ CDD

☐ 1: ZP_03049943. Reports NADP-specific glu...[gi:193068984]

BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS ZP_03049943 447 aa linear BCT 25-JUN-2008
 DEFINITION NADP-specific glutamate dehydrogenase [Escherichia coli E110019].
 ACCESSION ZP_03049943
 VERSION ZP_03049943.1 GI:193068984
 DBSOURCE REFSEQ: accession [NZ_AAJW02000011.1](#)
 KEYWORDS .
 SOURCE Escherichia coli E110019
 ORGANISM [Escherichia coli E110019](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 447)
 AUTHORS Rasko,D., Rosovitz,M., Myers,G., Seshadri,R., Cer,R., Jiang,L.,
 Ravel,J., Fricke,W.F. and Sebastian,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUN-2008) J. Craig Venter Institute, 9704 Medical
 Center Drive, Rockville, MD 20850, USA
 REFERENCE 2 ([residues 1 to 447](#))
 AUTHORS Rasko,D.A., Rosovitz,M.J., Kaper,J.B., Myers,G.S.A., Seshadri,R.,
 Cer,R.Z., Jiang,L. and Ravel,J.
 TITLE Direct Submission
 JOURNAL Submitted ([01-SEP-2005](#)) The Institute for Genomic Research, 9712
 Medical Center Drive, Rockville, MD 20850, USA
 COMMENT PREDICTED REFSEQ: This record has not been reviewed and the
 function is unknown. The reference sequence was derived from
[EDV88223](#).
 Escherichia coli E110019 was isolated from an outbreak in Finland
 (Viljanen MK et al, Lancet (1990), 336(8719): 831-4). The outbreak
 affected approximately 650 students at a school. In a fashion
 uncommon in other EPEC strains, E. coli E110019 spread from
 person-to-person to over 100 close contacts outside of the school
 setting. E. coli E110019 represents an atypical enteropathogenic E.
 coli (atypical EPEC) characterized by the lack of previously
 identified EPEC virulence factors including the EAF plasmid.
 E110019 is serotype O111:H9.
 Method: conceptual translation.
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 /db_xref="taxon:340186"
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 /calculated_mol_wt=48452
 Region
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 /region_name="PRK09414"
 /note="glutamate dehydrogenase; Provisional; PRK09414"
 /db_xref="CDD:103887"

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Region      57..187
             /region_name="ELFV_dehydrog_N"
             /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
             pfam02812"
             /db_xref="CDD:111682"
Region      202..445
             /region_name="NADB_Rossmann"
             /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
             /db_xref="CDD:127283"
CDS         1..447
             /gene="gdhA"
             /locus_tag="EcE110019_3311"
             /coded_by="complement(NZ_AA02000011.1:36581..37924)"
             /note="identified by match to protein family HMM PF00208;
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ORIGIN

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121  tlpmggkgg  sdfdpkgkse  gevmrfoqal  mtelyrhlga  dtdvpagdig  vggrevvgfma
181  gmmkklsnnt  acvftgkgl  fggslirpea  tgyglvyfte  amlkrhgmgf  egmrsvsvgs
241  gnvagyaiek  amefgarvit  asdssgtvvd  esgftkekla  rlieikasrd  grvadyakef
301  glvylegqgp  wsvvpdialp  catqneldvd  aahqliangv  kavaeganmp  ttieatelfq
361  qagvlfapgk  aanaggvats  glemaagaa  lgwkaekvda  rlhhimldih  hacvehggeg
421  eqtnyvqgan  lasfvkvada  mlaqgvi

```

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to Features: ☒ CDD

☐ 1: [YP_001463059](#). Reports [glutamate dehydro...](#) [[gi:157158996](#)]

[BLink](#), [Conserved Domains](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS YP_001463059 447 aa linear BCT 25-JUL-2008
 DEFINITION glutamate dehydrogenase [Escherichia coli E24377A].
 ACCESSION YP_001463059
 VERSION YP_001463059.1 GI:157158996
 DBSOURCE REFSEQ: accession [NC_009801.1](#)
 KEYWORDS .
 SOURCE Escherichia coli E24377A
 ORGANISM [Escherichia coli E24377A](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 447)
 CONSRSTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-2007) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 2 (residues 1 to 447)
 AUTHORS Rasko,D.A., Rosovitz,M.J., Brinkley,C., Myers,G.S.A., Seshadri,R.,
 Cer,R.Z., Jiang,L. and Ravel,J.
 TITLE Direct Submission
 JOURNAL Submitted (13-AUG-2007) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [ABV20734](#).
 Source DNA and bacteria available from Jacques Ravel
 ([jravel@tigr.org](#)).
 Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /strain="E24377A"
 /db_xref="taxon:331111"
 Protein 1..447
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 Region 6..447
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 Region 57..187
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 /db_xref="CDD:111682"
 Region 202..445
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 /note="Rossmann-fold NAD(P)(+)-binding proteins; c109931"
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NADPH; forms a homohexamer"  
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ORIGIN

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1  mdqtyslesf  lnhvqkrdpn  qtefaqavre  vmttlwfpfe  qnpkyrqmsl  lerlveperv  
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241  gnvagyaiek  amefgarvit  asdssgtvvd  esgftkekla  rlieikasrd  grvadyakef  
301  glvylegqqp  wsvpvdialp  catqnelvdv  aahqliangv  kavaeganmp  ttieatelfq  
361  qagvlfapgk  aanaggvats  glemaqnaar  lgwkaekvda  rlhhimldih  hacvehggeg  
421  eqtnyvqgan  iagfvkvada  mlaqgvi
```

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☐ 1: [YP_002407302](#). Reports [glutamate dehydro...](#)[gi:218699673]

BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS YP_002407302 447 aa linear BCT 22-DEC-2008
 DEFINITION glutamate dehydrogenase, NADP-specific [Escherichia coli IAI39].
 ACCESSION YP_002407302
 VERSION YP_002407302.1 GI:218699673
 DBSOURCE REFSEQ: accession [NC_011750.1](#)
 KEYWORDS .
 SOURCE Escherichia coli IAI39
 ORGANISM [Escherichia coli IAI39](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 447)
 CONSTRM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (18-DEC-2008) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 2 (residues 1 to 447)
 AUTHORS Genoscope -, C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-2008) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [CAR17428](#).
 Annotation results relative to BLAST similarities, COG
 assignments, enzymatic function prediction (PRIAM software), TMHMM
 and SignalP predictions, and syntenic conservation (Syntonyzer
 software) are available in the MaGe annotation system
<http://www.genoscope.cns.fr/agc/mage>.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /organism="Escherichia coli IAI39"
 /strain="IAI39"
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 Protein 1..447
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 Region 6..447
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 Region 57..187
 /region_name="ELFV dehydrog_N"
 /note="Glu/Leu/Phe/Val dehydrogenase, dimerisation domain;
 pfam02812"
 /db_xref="CDD:111682"

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ORIGIN

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121 tlpmggkgkg sdfdpkgkse gevrmfcqal mtelyrhlg dtdvpagdig vggrevgfma
181 gmmkkksnnt acvftgkgl fggslirpea tgyglvyfte amlkrhgmge egmrsvsvgs
241 gnvagyaiek amefgarvit asdssgtvvd esgftkekla rlieikasrd grvadyakef
301 glvylegqqp wsvpvdialp catqneldvd aahqliangv kavaeganmp ttieatelfq
361 gagvlfapgk aanaggvats glemagnaar lgwkaekvda rihhimldih hacvehggeg
421 dqtnyvqgan iagfvkvada mlsqgvi

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